

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTTTGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
 1 5 10

Leu	Ile	Ser	Gly	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala		
270						275					280						
GGG	ATT	ACA	GGC	GTG	AGC	CAC	CAC	GCC	CGG	CTT	ATT	TTT	AAT	TTT	TGT	914	
Gly	Ile	Thr	Gly	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys		
285					290					295					300		
TTG	TTT	GAA	ATG	GAA	TCT	CAC	TCT	GTT	ACC	CAG	GCT	GGA	GTG	CAA	TGG	962	
Leu	Phe	Glu	Met	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp		
				305					310					315			
CCA	AAT	CTC	GGC	TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	CTC	AAG	CGA	TTC	1010	
Pro	Asn	Leu	Gly	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe		
			320					325					330				
TCC	TGT	CTC	AGC	CTC	CCA	AGC	AGC	TGG	GAT	TAC	GGG	CAC	CTG	CCA	CCA	1058	
Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro		
			335				340					345					
CAC	CCC	GCT	AAT	TTT	TGT	ATT	TTC	ATT	AGA	GGC	GGG	GTT	TCA	CCA	TAT	1106	
His	Pro	Ala	Asn	Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr		
	350					355					360						
TTG	TCA	GGC	TGG	TCT	CAA	ACT	CCT	GAC	CTC	AGG	TGACCCACCT	GCCTCAGCCT	1159				
Leu	Ser	Gly	Trp	Ser	Gln	Thr	Pro	Asp	Leu	Arg							
365					370				375								
TCCAAAGTGC	TGGGATTACA	GGCGTGAGCC	ACCTCACCCA	GCCGGCTAAT	TTAGATAAAA	1219											
AAATATGTAG	CAATGGGGGG	TCTTGCTATG	TTGCCCAGGC	TGGTCTCAA	CTTCTGGCTT	1279											
CATGCAATCC	TTCCAAATGA	GCCACAACAC	CCAGCCAGTC	ACATTTTTTTA	AACAGTTACA	1339											
TCTTTATTTT	AGTATACTAG	AAAGTAATAC	AATAAACATG	TCAAACCTGC	AAATTCAGTA	1399											
GTAACAGAGT	TCTTTTATAA	CTTTTAAACA	AAGCTTTAGA	GCA		1442											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Asn	Gly	Ala	Ile		
1				5					10					15			
Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala		
			20					25					30				
Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	Thr	His	Ala	Arg		
			35				40					45					
Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	Leu	His	Val	Gly		
	50					55					60						
Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	Ser	Val	Ser	Ala		
	65				70				75					80			
Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	Arg	Leu	Cys	Leu		

AAT Asn	GGC Gly	GCA Ala	ATC Ile	TCA Ser	GCT Ala	CAC His	CGC Arg	AAC Asn	CTC Leu	CGC Arg	CTC Leu	CCG Pro	GGT Gly	TCA Ser	AGC Ser	98
15 20																
GAT Asp	TCT Ser	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CCA Pro	GTA Val	GCT Ala	GGG Gly	ATT Ile	ACA Thr	GGC Gly	ATG Met	TGC Cys	146
30 35 40																
ACC Thr	CAC His	GCT Ala	CGG Arg	CTA Leu	ATT Ile	TTG Leu	TAT Tyr	TTT Phe	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GAG Glu	TTT Phe	194
45 50 55																
CTC Leu	CAT His	GTT Val	GGT Gly	CAG Gln	GCT Ala	GGT Gly	CTC Leu	GAA Glu	CTC Leu	CCG Pro	ACC Thr	TCA Ser	GAT Asp	GAT Asp	CCC Pro	242
65 70 75																
TCC Ser	GTC Val	TCG Ser	GCC Ala	TCC Ser	CAA Gln	AGT Ser	GCT Ala	AGA Arg	TAC Tyr	AGG Arg	ACT Thr	GGC Gly	CAC His	CAT His	GCC Ala	290
80 85																
CGG Arg	CTC Leu	TGC Cys	CTG Leu	GCT Ala	AAT Asn	TTT Phe	TGT Cys	GGT Gly	AGA Arg	AAC Asn	AGG Arg	GTT Val	TCA Ser	CTG Leu	ATG Met	338
95 100 105																
TGC Cys	CCA Pro	AGC Ser	TGG Trp	TCT Ser	CCT Pro	GAG Glu	CTC Leu	AAG Lys	CAG Gln	TCC Ser	ACC Thr	TGC Cys	CTC Leu	AGC Ser	CTC Leu	386
110 115 120																
CCA Pro	AAG Lys	TGC Cys	TGG Trp	GAT Asp	TAC Tyr	AGG Arg	CGT Arg	GCA Ala	GCC Ala	GTG Val	CCT Pro	GGC Gly	CTT Leu	TTT Phe	ATT Ile	434
125 130 135																
TTA Leu	TTT Phe	TTT Phe	TTA Leu	AGA Arg	CAC His	AGG Arg	TGT Cys	CCC Pro	ACT Thr	CTT Leu	ACC Thr	CAG Gln	GAT Asp	GAA Glu	GTG Val	482
145 150 155																
CAG Gln	TGG Trp	TGT Cys	GAT Asp	CAC His	AGC Ser	TCA Ser	CTG Leu	CAG Gln	CCT Pro	TCA Ser	ACT Thr	CCT Pro	GAG Glu	ATC Ile	AAG Lys	530
160 165 170																
CAT His	CCT Pro	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CAA Gln	GTA Val	GCT Ala	GGG Gly	ACC Thr	AAA Lys	GAC Asp	ATG Met	CAC His	578
175 180 185																
CAC His	TAC Tyr	ACC Thr	TGG Trp	CTA Leu	ATT Ile	TTT Phe	ATT Ile	TTT Phe	ATT Ile	TTT Phe	AAT Asn	TTT Phe	TTG Leu	AGA Arg	CAG Gln	626
190 195 200																
AGT Ser	CTC Leu	AAC Asn	TCT Ser	GTC Val	ACC Thr	CAG Gln	GCT Ala	GGA Gly	GTG Val	CAG Gln	TGG Trp	CGC Arg	AAT Asn	CTT Leu	GGC Gly	674
205 210 215 220																
TCA Ser	CTG Leu	CAA Gln	CCT Pro	CTG Leu	CCT Pro	CCC Pro	GGG Gly	TTC Phe	AAG Lys	TTA Leu	TTC Phe	TCC Ser	TGC Cys	CCC Pro	AGC Ser	722
225 230 235																
CTC Leu	CTG Leu	AGT Ser	AGC Ser	TGG Trp	GAC Asp	TAC Tyr	AGG Arg	CGC Arg	CCA Pro	CCA Pro	CGC Arg	CTA Leu	GCT Ala	AAT Asn	TTT Phe	770
240 245 250																
TTT Phe	GTA Val	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GGG Gly	TTC Phe	ACC Thr	ATG Met	TTC Phe	GCC Ala	AGG Arg	TTG Leu	ATC Ile	818
255 260 265																
TTG ATC	ATC ATC	TCT GGA	CCT TGT	TGT GAT	CTG CCT	GCC TGC	CGC GCC	TGC GCC	TCC CAA	AGT GCT						866

85					90					95					
Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp
			100					105					110		
Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	Pro	Lys	Cys	Trp
			115					120					125		
Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	Leu	Phe	Phe	Leu
			130					135					140		
Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	Gln	Trp	Cys	Asp
								150					155		160
His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala
				165					170					175	
Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp
			180					185					190		
Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser
			195					200					205		
Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro
			210					215					220		
Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser
			225						230						240
Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu
				245					250						255
Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly
			260					265						270	
Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly
			275					280					285		
Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met
				290				295					300		
Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly
				310									315		320
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser
				325					330					335	
Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn
				340				345						350	
Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp
			355					360					365		
Ser	Gln	Thr	Pro	Asp	Leu	Arg									
			370					375							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA 180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCCCA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCCTC 300
TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCCTGA GTTGCCCCA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC 420
GTGCTGGCC TTTTATTTT ATTTTITTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTITGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCTG CCTCGGCCA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
CTATTTTTAA TTTTGTITG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGTATT	TTTTTTTAGT	180
AGAGATGGAG	TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCC	GCCTCTGCCT	300
GGCTAATTTT	TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCCTCA	GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTTT	ATTTTATTTT	TTTAAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTTTAT	600
TTTTATTTTT	AATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GCGCAATCTT	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAGTTATTCT	CCTGCCCCAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATTTTT	TTGTATTTTT	780
AGTAGAGATG	GGGTTTCACC	ATGTTGCCCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
CTGCCTGCCT	CGGCCTCCCA	AAGTGCTGGG	ATTACAGGAC	GTGACGCCCC	CCGCCC GGCC	900
TATTTTTAAT	TTTTGTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCCA	AGCAGCTGGG	ATTACGGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTTGTATT	1080
TTCATTAGAG	GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACCTC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCACAG	1200
CGGCTAATTT	AGATAAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAAC	TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTTAAAC	AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
AACCTGCAAA	TTGAGTAGT	ACAGAGTCTT	TTATAACT			1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

CCAGGTGTAG NCCA